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(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

## (57) Abstract

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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## COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spittler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95% identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### Example 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

**Example 2****DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR  
POLYPEPTIDES**

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### Example 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun  
Dillin, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
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(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.427C3

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT	TTTTTCACAG	TATAACAGCT	CTTTATTCT	GTGAGTTCTA	CTAGGAAATC	60
ATCAAATCTG	AGGGTTGCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTAACCTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCAGCG	GTGGAGCTCC	AGCTTTAGTG	CCCTTTAGTG	AGGGTTAATT	420

GCGCGCTTGG CGTAATCATG GTCATAACTG TTTCCGTGT GAAATTGTTA TCCGCTCACA	480
ATCCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGTGC CTAATGAGTG	540
ANCTAACTCA CATTAAATTGC GTTGCCTCA CTGNCCGCTT TCCAGTCNGG AAAACTGTCG	600
TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCGGGGAAAA GCGGTTGCG TTTGGGGC	660
TCTTCCGCTT CTCGCTCACT NANTCCGTGCG CTGGTCNTT CGGCTGCCGG GAACGGTATC	720
ACTCCTCAAA GGNGGTATTA CGGTTATCCN NAAATCNGGG GATAACCNNGG AAAAANTTT	780
AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA	814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT TGGATGGTGG AGCACCTTTC TATACGACTT ACAGGACAGC AGATGGGAA	60
TTCATGGCTG TTGGAGCAAT AGAACCCAG TTCTACGAGC TGCTGATCAA AGGACTTGGG	120
CTAAAGTCTG ATGAACTTCC CAATCAGATG AGCATGGATG ATTGCCAGA AATGAAGAAG	180
AAGTTGCAAG ATGTATTTGC AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC	240
ACAGATGCCT GTGTGACTCC GGTCTGACT TTTGAGGAGG TTGTTCATCA TGATCACAAAC	300
AAGGAACGGG GCTCGTTAT CACCAGTGAG GAGCAGGAGC TGAGCCCCCG CCCTGCACCT	360
CTGCTGTTAA ACACCCAGC CATCCCTCT TTCAAAAGGG ATCCACTAGT TCTAGAACG	420
GCCGCCACCG CGGTGGAGCT CCAGCTTTG TTCCCTTTAG TGAGGGTTAA TTGCGCGCTT	480
GGCGTAATCA TGGTCATAGC TGTTCTGT GTGAAATTGT TATCCGCTCA CAATTCCCCC	540
AAACATACGAG CCGGAACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN	600
CATTAATTGC GTTGCCTCA CTGCCGCTT TCCAGTCGGG AAAACTGTCG TGCCACTGCN	660
TTANTGAATC NGCCACCCCC CGGGAAAAGG CGGTTGCNTT TTGGGCCTCT TCCGTTTCC	720
TCGCTCATG ATCCTNGNC CCGGTCTTCG GCTGCGGNGA ACGGTTCACT CCTCAAAGGC	780
GGTNNTCCCG TTATCCCCAA ACNGGGATA CCCNGA	816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG AAGGGATGGC TGGGGTGTAA AACAGCAGAG GTGCAGGGCG GGGGCTCACG	60
TCCTGCTCCT CACTGGTGTAA AACAGGCC CGTTCCTGTG TGTGATCATG ATGAACAAAC	120
TCCTCAAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCCAC	180
TCTGCCTTCG TCTTCTTGC AAATACATCT GCAAACCTCT TCTTCATTTG TGCCAAATCA	240
TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC CANNCTCTT GATCAGCAGC	300
TCGTTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCCTCTGC TGTCCCTGTAA	360
GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTCGAGGGGG GGCCCGGTAC	420
CCAATTGCC CTATANTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC	480
GTGACTGGGA AAACCCCTGGG CGTTACCAAC TTAATCGCCT TGCAAGCACAT CCCCCTTCG	540
CCAGCTGGC GTAATANCAGA AAAGGCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT	600
GAATGGGNA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCCNNGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTGCCTA GCGCCTTANC GCGCGCTCCC TTTCNCTTT	720
CTTCCCTTCC TTTCNCCCN CTTTCCCCCG GGGTTCCCG CNTCAAACCC CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCCT	360
GNNGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAACATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCACACAC	ACATACGANC	CGGAAACATA	AANTGTAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCCGTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCAT	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	GTTCGCTTT	TGGGCGCTCT	720
TCCGCTTCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	CGGCTGCNGC	AAACCGGTTTC	780
ACCNCCTCCA	AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAAG	TACTAACAA	AACTCTAGCA	ATCAAGAAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACCC	TGTGGCTTT	AAAATTTGGT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240
ACATTTGGCA	TAAACAATAA	AAAAACAATC	ACAATTTAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATAA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	360
AATAGAATAC	CTTGGCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTAC	TCAGCCCTGA	420
CATTCACTTT	TCAAAGTAGG	AGACAGGTT	TACAGTATCA	TTTTACAGTT	TCCAACACAT	480
TGAAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTAATG	CATTACATCC	TCAAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTC	AAAGTTTATATT	AGTCATATAA	CTTGGTGTGC	600
TTATTTTAAA	TTAGTCCTAA	ATGGATTAAG	TGAAGACAAC	AATGGTCCCC	TAATGTGATT	660
GATATTGGTC	ATTTTTACCA	GCTTCTAAAT	CTNAACTTT	AGGCTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TGTTATTTTG	TTAAAAAATTA	AAATTAAACC	TGGTGGAAAA	ATAATTGAA	ATNA	834

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCCCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTGGA	120
TGTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CGCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGGTAAAAT AGAGACCCAG	300
TAAAATTGTA ATAAGCACTG CTTGAATTAT TTGGTTTCGG TTGTTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCCCTGATGC GAGTAAATACG GATGTTGTTA GGAGTGGGAC	420
TTCTAGGGGA TTAGCGGG TGATGCGT TGCGGGCCAG TGCCCTCCTA GTTGGGGGGT	480
AGGGGCTAGG CTGAGACTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA	540
GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGT TTACATCGCG CCATCATGG TATATGGTTA GTGTGTTGG	660
TTANTANGGC CTANTATGAA GAACTTTGG ANTGGAAATTA AATCAATNGC TTGGCQGGAA	720
GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGCTGGG CTNGGTTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTAA	818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAGATT TTAGGGGA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTTCAGA GAGCATTGAC CGTAGTATAC CCCCCGGTCGT GTAGCGGTGA	180
AAGTGGTTTG GTTTAGACGT CCGGGAAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG	240
CTCATGAGTG CAAGGACGTCT TGTGATGTA TTATTATACN AATGGGGGCT TCAATCGGGA	300
GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG	360
GAAGTATGTA GGAATTGAGG ATTAATCCGC CGTAGTCGGT GTTCTCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTTC ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTAA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTTCCT GAAACGTCG AAATGTTAAT AANAATTAAN TTTNGTTATT	600
GAATTTINNG GAAAAGGGCT TACAGGACTA GAAACCAAT ANGAAAANTA ATNNNTAANGG	660
CNTTATCNTR AAAGGTNATA ACCNCTCTA TNATCCCACC CAATNGNATT CCCCACNCCN	720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC	780
CTTNANTGAN GGTTATTNC CCCTNGCNTT ATCANCC	817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120

CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCG CGTCCTGGG	240
TGGGTGCCG ANGCTGANC CGCTCTGCCT TGCTGCCCTC ANGTGGGCCG CCACCCCTG	300
ACCTGCCTGG GTCCAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG	360
GGATTTGCT CCTANANTAA GGCTCATCTG GGCTCGGCC CCCCACCTG GTTGGCCTTG	420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTT NGGGAGTGT	480
CTCTTACAA CCACANNATG CCCGGCTCCT CCCGGAAACC ANTCCCANCC TGNGAAGGAT	540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAACCC NCNCTTNTGT	600
TCCTTTCTNT TNAGGGTTAA TNNGCCTTG GCCTTNCCAN NGTCCNCNC NTNTTCCNN	660
GTTNAATTG TTANGCNCC NCCNNTCCCN CNNCNNCNAN CCCGACCCNN ANNTTNNANN	720
NCCTGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT TGCNTTNGGG NNCNNTGCC	780
CTTCCCTCT NGGGANNCG	799

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTG	60
TAANGATGAC ACTCCCAAAG GTGGCTCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT GCGGGGCCG AAGCCCACAT GATCCTTACT CTATGAGCAA	180
AATCCCTGTG GGGGGCTCTC CCTTGAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG	240
CAGGTATGG GGTTGTGNC CAACTGGGG CCNCAACGCA AAANGGCNA GGGCTCNGN	300
CACCCATCCC ANGACCGGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGGCCTG	360
TTCTNTACCCG CGNATNTGTC CCANCTGTTT CNGTGCNAAC TCCANCTCT NGGACGTGCG	420
CTACATACGC CCGGANTCNC NCTCCCGCTT TGTCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG CACNNTTNNC AGNTTTCCNC NNCGNGCTTC CTTNTAAAAG	540
GGTTGANCCC CGGAAATTC CCCAAAGGGG GGGGGCCNGG TACCCAACTN CCCCTNATA	600
GCTGAANTCC CCATNACNN GNCTCNATGG ANCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTAA TCCCNCTTG CNANGNNCNT CCCCNNTCC	720
NCCNNNTNG GCNTNTNANN CNAAAAAGGC CCNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGA GAAGCAGGTG TTCCCTGCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCCTCCCTA ATGGACACGT GGGTGCTGGA GGCAGTGGCC	300
TGCTCCACC TCCACCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGTCTC TGCTGCTCCA NGTGGCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCGCGAGGCC TGGGCTGGT	540

CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC	660
TCCTGTTAAC CCCATGGGGC TGCCGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGTNG	780
GGNGTTCCCC	789

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTT AATATTAAA TGCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCTCA GGACTCTTC CCTACAAATA	240
ACTTCATAT GTTCAAATCC CATGGAGGAG TGTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTTAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTAGCTC CAAAAAACCC TTCTCTAGGT GTGTCTAAC TAGGAGGCTA GCTGTTAAC	420
CTGAGCCTGG GTAATCCACC TGAGAGTCC CGCATTCCA GTGCATGGAA CCCTCTGGC	480
CTCCCTGTAT AAGTCCAGAC TGAAACCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA	540
AACTGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCACTACG CACCTCAACA	600
GCACAGGTG GCAGCAAAAA AACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGGCA	660
ACCCGGCAC CCCNANGGG GTTAACAGGA ANCNGGGNAA CNTGGAACCC AATTNAGGCA	720
GGCCCNCCAC CCCNAATNTT GCTGGGAAAT TTTCTCCCC CTTAATNTT TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTG CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCCCTC TACTTTTGG TCGTGAGCCT TTTGCTTGGT GCAGGTTTCA	120
TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACT GTTCTCTTG	180
AAGTANGTGT AGTCCTCAAAT ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA	300
GGCACTACCA GCAAGCTCAG GGAAGTGTCT AGCCATTGTG GTGTACACCA AGGCGACCAC	360
AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGGANGATG AAGAAGAACG TCNCGAGGGC	420
ACACTTGCTC TCACTCTTAN CACCATANCA GCCCNTGAAA ACCAANANCA AAGACCAACNA	480
CNCCGGCTGC GATGAAGAAA TNACCCNCG TTGACAAACT TGCACTGGCAC TGGGANCCAC	540
AGTGGCCCNAAAATCTCA AAAAGGATGC CCCATCNATT GACCCCCCAA ATGCCCACTG	600
CCAACAGGGG CTGCCACCN CNCNNAAACGA TGACCNATT GNACAAAGATC TNCNTGGTCT	660
TNATNAACNT GAACCTTGCN TNGTGGCTCC TGTCAGGNC CNNGGCCTGA CTTCTNAANN	720
AANGAACTCN GAAGNCCCCA CNGGANANN G	751

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CGGGGAGCTG	TTTTGTCCCTT	60
TGTGGANCT	CAGCAGTNCC	CTCTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCATAATT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGTAAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTTT	600
GAAGANTCAC	CTACTTCAAA	GAAAANAGTG	CCTTTCCCCC	ATTTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGTCC	CCAACCANAA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 816 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCA	TAACAACCC	CATAGGTAAA	GCGGGGCGAG	60
TGTCGCTGA	AGGGGTTGTA	GTACCAAGCGC	GGGATGCTCT	CTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCC	TTTGTCACTG	GGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAAC	GGTGGGCTGA	300
CANGTGCCAG	AGCACACTGG	ATGGCGCTT	TCCATGNNA	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGACACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCNNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGGG	TCNTANTACC	ANC GTGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGNNNANC	TTAGNCCNTG	GTCCCTCNGG	GTGNNNCTTG	AACCTAATCN	CCNNNTCAACT	660
GGGACAAGGT	AAANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAA	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTTNTTC	780
CACAACCCTN	CCCCACCCAC	GGGTTCNGNT	GGTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 783 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGACTAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTGCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGGTG	420
TGCAAGGTGG	GCCTTTGANA	NGCANCTCTG	GGGCTCANGC	GACTIONTCCCC	CAGGGCCCT	480
CCATGGAAAG	GGCCATCNA	NTGTTCTCTG	GCACCTGTCA	GCCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTNAAAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCGG	660
CNCCTCCNTT	TTCCCCNNNT	AAACAAAGGGC	NCTNGCNTTT	GAACTGCCCN	AAACCCNGGAA	720
TCTNCCNNGG	AAAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNA	ANCTNCCCCC	780
CCC						783

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAAGTCAG	GAAGTGTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTGTGCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAA	GACCACAAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACGTG	600
CNACAGGGCT	GCNCCNCNCN	AAAGAAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACATGAAA	CCTGTCATGG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCN	G				801

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTG	60
CCTTGTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTC	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTGTC	CAGTGCCTAG	CAGTTTGTC	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCCTGGGCT	GCTATGGTGC	360

TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTCGCCCTT GGTGTACACC ACAATGGCTG AACCATTCCT	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATACCG	600
GAATTTGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCTTTNCC CCCNTCTGT	660
TGCAATGAAA ACNTCCCAA ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNAAA	720
CAAAAAAANT NNAAGGGTTN	740

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATAACACA GCCTCAATCA	60
CAAGGTCTTC CAGCTGCCG ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG	120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT	180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCAT	240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA	300
CATTGGGCAT GTCCAGCAGT TCTCCAAACAA CGTAGACACC AGNGGCCTCC AGCACCTGAT	360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CGCACTTGGC TAGGAGCAGA ATTGCTCCT	420
GGTTCTGCCCG TGTCACTTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG	480
GCTCAGGATG TCCAGAGACG TGGTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC	540
GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAAGG GTCTGCTGGC CNCTACTTGC	600
AANCTTCGTC NGGCCCATGG AATTCAACCNC ACCGGAACTN GTANGATCCA CTNNTTCTAT	660
AACCGGNCGC CACCGCNNTT GGAACTCCAC TCTTNTTNCC TTTACTTGAG GGTTAAGGTC	720
ACCCCTNNCG TTACCTTGTT CCAAACCTN CCNTGTGTG ANATNGTNAA TCNGGNCCNA	780
TNCCANCCNC ATANGAAGCC NG	802

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC AGGTNACGGG CGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG	60
GAGCCCCACCG TCACGNNGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT	120
CNTGACCCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG	180
CAGGAACCAA GANCAAANN NCAGCTCCNNT CAAGTCGGCN NAGGGGGCGG GGCTGCCAC	240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGCENNNA	300
CATGCCCAAGN GTTANATAAC NGGCNGAGAG TNANNTTGCC TCTCCCTTCC GGCTGCGCAN	360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAAGTGAA CCCNNGAATC TNCCNCCCT	420
CCACTAAGCT CAGAACAAAA AACCTCGACA CCACCTCANTT GTCACCTGNC TGCTCAAGTA	480
AAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG	540
GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC	600
CNNCNNTCCA AGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN	660
CCCCCNNGCC CGGCCCTTTA CNANCNTCNN NNACNGGNA AAACCNNGC TTNCCCAAC	720
NNAATCCNCC T	731

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC	60
CAACCCCCCTC NTCAAATNN CCNTTCCGG GNGGGGGTTC CAAACCCAAN TTANNTTTGG	120
ANNTTAAATT AAATNTTNNT TGGNGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA	180
TNANCCTNAA TNCCCTGGAAA CCNGTNGNTT CCAAAAATNT TTAACCCCTTA ANTCCCTCG	240
AAATNGTTNA NGGAAAACCC AANTTCTCT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC	300
NNCCAATTGT TTTTNGGCCAC GCCTGAATTA ATTGGNTTCC CNTGTTTCC NTTAAAANAA	360
GGNNANCCCC GGTTANTNAA TCCCCCNNC CCCAATTATA CCGANTTTT TTNGAATTGG	420
GANCCNCGG GAATTAACGG GGNNNNNTCCC TNTTGGGGGG CNGGNCCCC CCCCNCTCGG	480
GGTTNGGGNC AGGNCCNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC	540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTGG	600
GGGGCCTGGG ATTTNTTTTC CCCTNTTNCC TCCCCCCCCC CCNGGGANAG AGGTTNGNGT	660
TTTGNTCNNC GGCCCCNCCN AAGANTTT CCGANTTNAN TAAATCCNT GCCTNGGCAG	720
AGTCCTTGN AGGGNTAAAN GGCCCCCTNN CGGG	754

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT GACCCCNAAC NNNGGACNC TCANCCGGNC NNNCNACCNC CGGCCNATCA	60
NNGTNAGNNC ACTNCNNTTN NATCACNCCC CNCCNACTAC GCCCNANC CNACGCNCTA	120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN	180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCTC CNAAGTATTN	240
NNCNANCNAT GATTTCTTN ANCCGATTAC CCNTNCCCCC TANCCCTCC CCCCCAACNA	300
CGAAGGCNCT GGNCNAAGG NNCGNCNCC CCGCTAGNTC CCCNNCAAGT CNCNCNCTA	360
AACTCANCCN NATTACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC	420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT	480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATT CCNAANGGCT	540
CTTTCNGACA GCATNTTTG GTTCCNNTT GGGTTCTTAN NGAATTGCCC TTCNTNGAAC	600
GGGCTCNTCT TTTCCTTCGG TTANCCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNTTTT	660
AAATTCTNCC CNTTANTTT TGGCNTTCNA AACCCCCGGC CTTGAAAACG GCCCCCTGGT	720
AAAAGGTTGT TTGANAAGA TTTTGTGTTT GTTCC	755

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACTTC	GGCGGGCCNG	NGNCCGGGGC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCCN	NCCCCNNCNG	ACCCNNGGGA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAAATGGG	CCNCGGNNCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGGACT	GCCNANNNGCT	CCGTTNCTNG	420
NNACCCCCNN	GGGTNCTCG	GTTGTCGANT	CNAACCGNANG	CCANGGATTC	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCCTACCC	TCGCTNCGG	NNCACCCCTTC	CCGACNANGA	NCCGCTCCCG	540
CNCNNCGNNG	CCTCNCTCG	CAACACCCGC	NCTCNCNTG	NCGGNNNNCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GGNCNCNCC	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNA	CNAAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCCGN	CTTCCNACCC	ANGNNNTCCN	CGAGGACACN	NNACCCC GCC	840
NNCANGCGG						849

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCCTCC	ANAGTANACN	ATTGAACNNG	AGAACCCANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTGGGA	300
TCGGGTTTNN	NNTGACCNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCAACC	360
NANNGCNCG	NCCCCGNNCT	CTTCGCGNCC	CTGCTCTNTN	CCCCGTGNGC	CTGGCNCNGN	420
ACCGCAATTGA	CCCTCGCCNN	CTNCNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCCTG	480
TGGGNNNGCG	TCTGCNCCGC	GTTCCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCNTC	TCTNNCACNC	CCTGGGACGC	TNTCTNTGC	CCCCCTTNAC	CCCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCANCCNAG	GGAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCGG	NGNGCNCNTC	TCAGGCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNNTAC	GANTNTTCGN	CNCCCTCTTT	CC			872

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATTC	TATAGNGTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCTNATNTGA	CAAGANNGTA	120

TCNTNCATTA	GTAACAANTG	TNNGTCCAT	CCTGTCNGAN	CANATTCCC	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGGAA	NTCNNTNNN	NCACNNCAT	CTATCNCC	240
GCNCCTGAC	TGGNAGAGAT	GGATNANTTC	TNNNTGACC	NACATGTTCA	TCTTGGATTN	300
AANANCCCC	CGCNGNCCAC	CGGTTNGNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATECCGTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCCCT	ANAGGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCC	AGNCCANCCG	CAATNGGCA	CAATGTCNC	540
GAACCCCCTA	GGGGGANTNA	TNCAAANCC	CAGGATTGTC	CNCNCANGAA	ATCCCNCANC	600
CCCNCCCTAC	CCNNCTTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCNCNTGGGG	GGGTGAANCT	CNGNNTCANC	CNGNCAGGNN	NTCGNAAGGA	720
ACCGGNCTN	GGNGAANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCCTCNCCA	780
NCCNACNGNT	AGNTCCCCCCC	CNGGGTNCGG	AANGG			815

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	CGGTACTCCA	AAGATTCAAGG	TTTACTCACG	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATT	TCTGAATTGC	TATGTGTCCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATT	AGACTTGTCT	TTCAGCAAGG	240
ACTGGCTTT	CTATCTCNTG	TACTACACTG	AATTCAACCC	CACTGAAAAAA	GATGAGTATG	300
CCTGCCGTG	GAACCATGTG	ACTTTGTCAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTITGAAGAT	GCCGCATTG	GATTGGATGA	ATTCCAATT	420
CTGCTTGCTT	GCNTTTTAAT	ANTGATATGC	NTATACACCC	TACCTTTAT	GNCCCCAAAT	480
TGTAGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAAANT	CCNCCNTTCG	540
AATTGCCGT	CNCCCNCGTTN	NGAATGTTTC	CNNAACCACG	GTTGGCTCCC	CCAGGTCNCC	600
TCTTACCGAA	GGGCCTGGGC	CNCTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTTNGC	660
CCNCCCNCCA	CNNTCTTGNG	NNCNCANTTT	GGAACCCCTTC	CNATTCCTCC	TGGCCTCNNA	720
NCCTTNCTA	ANAAAACTTN	AAANCNTNGC	NAAANNTTTN	ACTTCCCCCC	TTACC	775

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAATCT	TTTCCCAGAG	GTGTGTANAG	CGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTCCTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGCGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCCTACCTG	ACNACCAGNG	ACCNNAACT	GCNGCCTGGG	GACAGCNCCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCC	CCCAGGGCCG	TNCGNTCCC	TGGTCTGNC	AAGGAAAGCT	480
CCCTGTTGGA	ATTNCGGGGGA	NACCAAGGGA	NCCCCCTCCT	CCANCTGTGA	AGGAAAANN	540
GATGGAATT	TNCCCTTCCG	GCCNNTCCCC	TCTTCCTTTA	CACGCCCCCT	NNTACTCN	600

TCCCTCTNTT	NTCCTGNNC	ACTTTNACC	CCNNNATTTC	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNCGCCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCCNGGGAT	720
GGGNNCCTCG	NTCATCCTCT	CTTTTCNCT	ACCNCCNNTT	CTTTGCCTCT	CCTTNGATCA	780
TCCAACCNTC	GNTGGCCNTN	CCCCCCNNN	TCCTTTNCCC			820

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGGAA	CCTCTGACTG	CTCTGGGCCA	AAGAACATCTCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTCAAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCCTGCC	CAGCCCCCTGC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCCTGGG	CCACACTGGC	300
TTCTTCTCTGC	CCCNCTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACCTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNNNA	ACCNGCTNC	CNTCNTCTCC	CCNTANCCG	CCNGGAAANC	540
CTCCTTGC	CTNACCANGG	GCCNNNACCG	CCCNNTNCTN	GGGGGGCNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNNT	TNCCCTGTC	CNNCNNGCN	NNGCANNITC	NCNGTCCNN	660
TNNCTCTCN	NGTNTCGNAA	NGTNCNCTN	TNNNNNGCN	NGNTNNNTMCN	TCCCTCTCNC	720
CNNNTGNANG	TNNNTNNNNC	NCNGNNCC	NNNCNNNNN	NGGNNTNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNCT	CCGGCCNC			818

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGGTGTG	60
TCCAACATG	ANGGTGNNGT	TCTCTTTGA	ANGAGGGTTG	NGTTTTTANN	CCNGGTGGGT	120
GATNAACCC	CATTGTATGG	AGNNAAAGGN	TTTNAAGGGAT	TTTTCGGCTC	TTATCAGTAT	180
NTANATTCCCT	GTNAATCGGA	AAATNATNTT	TCNNCNGAA	AATNTTGCTC	CCATCCGNA	240
ATTNCTCCCG	GGTAGTGAT	NTTNGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGAN	TNCAAATGAA	AACTTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCT	TCGCCCCNTG	ACTCTGCNNG	AGCCAATAC	CCNNNGNAT	GTCNCCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNN	480
CGTTTCNCAT	NAAGGCACCT	TNGCCTCATC	CAACCNTNG	CCCTCNCCCA	TTTNGCGTC	540
NGGTTNCCT	ACGCTNNTNG	CNCCTNNNTN	GANATTTNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGT	GGGNCTTNTC	TTTNAACNN	GNGGTNTACT	AATCNCTNC	ACGCNTNCTT	660
TCTNACCCCC	CCCCCTTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGG	720
NNNCCCANNC	C					731

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNN	120
ATNTNTACNC	TCATANNCTC	CNNNACCCAC	TCCCCTTAA	CCCNTACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCGCCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAACNC	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTNC	ATNANCTCT	AATTGAAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TTCNCCAAAC	TTNNCCTCCG	ATCCCCNNAC	AACCCQCCCTC	480
CCAAATAACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCG	GCAAGCCNAM	GGNCATTTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCCNAT	CTCCCTAANA	600
AATNCTCTN	NAATTAACTN	NCANTNCAT	CAANCCACN	TGAAACNNAA	CCCCCTGTTT	660
TANATCCCTT	CTTTGAAAAA	CCNACCCCTT	ANNNCCCAAC	CTTTNGGGCC	CCCCCNCTNC	720
CCNAATGAAG	GNCNCCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGGNCCCTT	NCCCNNGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCGGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAAGTGATGGA	CTGCCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCCT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTGCCA	GCCTCCCCCT	TCTCTCCACC	CTCTCCANGG	240
ACACCAAGGGG	CTCCAGGCAG	CCCATATTTC	CCAGNANGAC	ATGGTGTTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCTT	TTGACACCAT	CTCTCCCCTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTTGT	420
TCCCNNTAAAT	GAAGGTTAAT	TGCNCCTTG	CGCTAATCAT	NGGTCANAAC	TNTTTCTGT	480
GTGAAATTGT	TTNTCCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCCTN	NGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTCCN	TTCNGGGAAA	CTGTCNTCCC	CTGCNTTNN	GAATCGGCCA	CCCCCNNGGG	660
AAAAGCGGTT	TGCNTTTTNG	GGGGNTCCCT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTGGC	GATGCTACTG	TTAATTGCA	GGAGGTGGG	GTGTGTAC	60
CATGTACAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCT	GNACANATC	CCTACGATTG	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCGG	GCCCACCTCT	CCNCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTG	480
CCTGGGCCCT	TAANTACCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTNNCNCT	CANCTAATGC	CCCCCCNGG	AACNATCCAA	CCCCCCCCCN	TGGGGCCCC	660
AGCCANGGC	CCCCGNCTCG	GGNNNNCGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGGGCG	GCGGGGGCG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTIN	AATTTCCACG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCC	AAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCCN	AAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCTTGGCC	CCCAAATCCT	CCCCCGNNT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGCAA	GNTGGNTCCC	CTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNAAGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTGGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAAGTTTC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTGAGGA	GGTTGTTCAT	CATGATCACA	300

ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTCAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAECT	600
NACTCACATT	AATTGGCTTT	GCGCTACTG	CCCCTTCC	AGTCCGGAAA	ACCTGTCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCAGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGA	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAACAG	CAGCTAATTG	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCTG	CTGTCCTCAGA	ACCGGGTGGC	TGANTNCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCATA	TNCACCA	420
GTGTCCTGG	GCAATACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAGGCTNC	AANAANATCC	TTTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCCCGCCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CTGTGTTGA	720
AATTNTTAAC	CCCCCACAAT	TCCACGCCNA	CATNG			756

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTTA	AGTTGCTAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAAA	300
CTTCTNNAAAN	ANGANNANCC	CANCTTGTG	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCCTGTC	TGCCTGCAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNCCNNG	CAGGGTTGGT	GGCANNCCGG	GCCCNCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGGCCG	GCNTCNCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCTTCCCC	CNCCCCNCGG	NGTTGGNTT	TTTCATNGGG	CCCCAACTCT	780

GCTNTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNNTNG GGCC

834

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCCCTGTA	180
GGAAAAGGCCT	GCCTTGTAAG	ACACCCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAAA	AAAATAAAC	AANAGGTTTT	GTTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAAG	ACCGGCCACC	480
AGGGGANGTC	NTTTNCAGTG	GATCTGCCAA	ANANTACCN	TATCATCNNT	GAATAAAAAG	540
GCCCCCTGAAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAG	GAATGTTCT	GGGTCCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCAAN	TGANATCCCC	NGAAGCACCC	TNCCCTGGC	720
ATTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGT	CGCTGAAGGG	GTTGAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGG	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATT	TTCACANGCA	GCCTCCTCCG	AAGCCTCCGG	GCAGTTGGGG	240
GTGTCGTCAC	ACTCCACTAA	ACTGTCGATN	CANAGCCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGC	TGGGGGAAAT	360
CNCCTNANCC	CAAACCTGCCT	CTAAAGGCC	ACCTTGCACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTGT	TGCCAAGCA	NCCTCCANCA	AACCAAANC	480
TTGCAAATC	TGCTCCGTGG	GGGTCACTNNN	TACCANGTT	GGGAAANAA	ACCCGGCNGN	540
GANCCNCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAAA	GGTANGTGGC	TTCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT TTTTTTTTTT TTTTTAAAAA CCCCCCTCCAT TGAATGAAAA	60
CTTCNAAAAT TGTCCAACCC CCTCNCCAA ATNNCCATT CCGGGGGGGG GTTCCAAACC	120
CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA	180
AATTAAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAAA ATTTTTAAC	240
CTTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGCCTT	300
NGATTTAAAC CCCCTPTNANT TNNTTTNACC CNNGNCTNAA NTATTNGNT TCCGGTGT	360
TCCNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNNCCT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGAATTNA CGGGGGTTT TCCCNNTTG GGGCCATNCC	480
CCCNCTTCG GGGTTTGGGN NTAGGTGAA TTTTNANG NCCCAAAAAA NCCCCAAANA	540
AAAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTTCCCA GGCCTTTG GAAAGGNGGG	600
TTTNNGGGGG CCNGGGANT CNTTCCCCN TTNCNCNC CCCCCCNNGGT AAANGTTAT	660
NGNNTTGGT TTTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAAT CCCCCGGNCG	720
GCCG	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTTCTTTG CTCACATTTA ATTTTTATTT TGATTTTTTT TAATGCTGCA	60
CAACACAATA TTATTTCTAT TTGTTCTTT TATTCATTT TATTTGTTTG CTGCTGCTGT	120
TTTATTTATT TTACTGAAA GTGAGAGGGA ACTTTGTGG CCTTTTTTCC TTTTTCTGTA	180
GGCCGCCCTTA AGCTTTCTAA ATTTGGAAC A TCTAAGCAAG CTGAANGGAA AAGGGGGTTT	240
CGAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTGTAA TCATGCCCTA TGGTGGGTGA	300
TTAAGTGTGTT GTACAATTAC NTTTCACTTT TAATTAAATTG TGCTNAANGC TTTAATTANA	360
CTTGGGGGTT CCCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCCGCNT CNTGAAACA CACNGCNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAAA	480
TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AATTNCTNNG CCCCGTNC GCNTNNGTCC CNCCCCGGGT CGGGGAANTN	600
CACCCCGNGA ANNCNNNTNC NAACNAAATT CCGAAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCNNCNAN CNAATTTC TTTTNTCAC GAACNCGNNC CNNAAAATGN	720
NNNCNCCTC CNCTNGTCCN NAATCNCCAN C	751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTCTT CTGTAAGATC AGGTGTTCTT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAAATGCCA AGCAGCCGG GTAGGAGGGG	120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA	180

TGGTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAAC	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGG	300
CGGTCAAAAN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGCNA	360
ATAAAAAGGTG	CGCCCCCGCA	CGGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGG	420
CNAACCCACC	ACCANNCCCG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCNGN	ATGCCAANCA	NCCCCAANCC	CCGGGGTCC	540
AAANCACCCN	CCTCCCTNNT	TCATCTGGGT	TNTNTCCCC	GGACCN	TGTTCTCAAG	600
GGANCCCATA	TCTCNACCAN	TACTCACCN	NCCCCCCCNT	GNNACCCANC	CTTCTAANGN	660
TTCCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCTATCT	GNACCCNCN	TTTGTCTCAN	TNT			753

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCCTTGATT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTTCCAC	120
TTCTTTAAC	CTTGTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTTAA	AAAATATCAT	TTGAGAATAT	TCTTTCAGAG	GTATTTTCAT	300
TTTTACTTTT	TGATTAATTG	TGTTTATAT	ATTAGGGTAG	T		341

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTGAT	60
GTTCAAACA	TTCTAAATAA	ATAATTTCA	GTGGCTTCAT	A		101

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTTCT TAAATCACCA TTCCCTCCTG GTCCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAGTAA GAGGACTTAA TATTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTCT	60
GATTATTTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC	120
CTCTCCATCC TCAGGGCATTC TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGTTTTCA TAGGTATGCA	240
TGCTGTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGCTTGC TCCTTTCTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTT CCAGGTGTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTTGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACCTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG	720
CCGGCCGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCGACAC CATCCGGAGC ATCAGCATTG CTTGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATT CACAGTTAAA	120
AAGAAGATAAA TATATTCCAA GCANATACAA AATATCTAAAT GAAAGATCAA GGCAGGAAAAA	180
TGANTATAAC TAATTGACAA TGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAAANAA TTATTGCACT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAAG GGGACAAAGG CTAATCCAA	240
AAACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGA CAACTGACCA TGTCAGG CTCCTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGTT ATATTCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCCCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT ATAAGGAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCTAGGAA GTCTAGGGAA CACACCACTC TGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCACCAC AGCCCTGCCA CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTAA AAACACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTCTT GTATCAATTCTT CTTTCTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAAATAA TCTCGTGAGA ACTTACCCACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420
CAATTTATT TGATAACAA AGGGCTCCA ATTATATTG AAAATAAAAT CCAAGTTAAT	480
ATCACTCTTG T	491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAAAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAA GTTCAGAAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAACGTT AAAAAGGT GTTGAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAANC	300
AGCTTTGANT TTCTTTGTC TGATANGAGG AAAGGCTGAA TTACCTTGTG GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAA CATATTCCAA CTCACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTTC CAGGANCAGG CGGATGGAAT GGGCAGCCC NC GGATGTT	480
CANT	484

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTTGTTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCCGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTATCCT TTAAAAAGA TGAAATCTT AATTTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCAITAA TGATTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCTCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGCGA TGCAANGGTG CCAACAGGAG	360
GGGGGGGAGG AGCATATG	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTG AGGGAAGAGA CTGTCGCCGTG CCTTCCTCCG TTGTTGCGTG	60
AGAACCCGTG TGCCCCCTTC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCCTGG TCCTCTCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT	180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTG CTTTGAGA CACTTGTCC CAGCACTTTA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTGAGAG AGTTCTCTC TGAGACCTGA TCTTTAGAGG	240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCATAC	360
CATAGTTTCT GTGCTAGTGG ACCGT	385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTTAA TGG	73

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

## (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGGCTC	TCACCCCTCCT	CTCCTGCAGC	60
TCCAGCTTTG	TGCTCTGCCT	CTGAGGAGAC	CATGGCCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCCGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCACCT	240
CGCCATCAGC	GAGTATAACA	AGGCCACCAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGGG	GGTGAATTAC	TTCTTCGACG	TAGAGGTGGG	360
CCGAACCATCA	TGTACCAAGT	CCCAGCCAA	CITGGACACC	TGTGCCCTTC	ATGAACAGCC	420
AGAACTGCAG	AAGAACAGT	TGTGCTTT	CGAGATCTAC	GAAGTCCCT	GGGGAGAAC	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCTAG	CCATGTGATT	60
TCACTTCCAC	TCCATAACCG	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTA	CACGAGAAAG	CACATACCA	GGCCACCCACA	CACCACCTGT	180
CCAAAAAGGC	CTTCGATACG	GGATAATCCT	ATTATTACC	TCAGAAGTTT	TTTTCTTCGC	240
AGGGATTTT	CTGAGCCTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGGCCCCC	AACAGGCATC	ACCCGCTAA	ATCCCCTAGA	AGTCCCAC	CTAAACACAT	360
CCGTATTACT	CCGATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATT	477

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTTCTACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGTA	AGAAAGAAAT	CACACCA	ATAATGGTA	GATTGGTTA	120
TGTGATTTA	GTGGTATTT	TGGCACCTT	ATATATGTT	TCCAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACCTAAA	AGTGAGTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAATAAAGG	TTTGTATCT	TTAAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCACTA	ATAATTATTA	GAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTG	CCTTGAAAAA	TATCAAATAT	AACTCTAGA	GAATGTACA	TAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTCCTC	CTCAATT	TATTTTAA	AAGTACATGG	480

TAAAAAAA AATTCAACAG AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC

533

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGTTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	AAAGAACAC	TAAAAGAGGG	ACAAGGCTAA	120
AAAGCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAAC	TGGTTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCTCC	GTCTGTTATG	420
ATTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAAG	NACCNGGAGG	A			511

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	GTAACTCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240
CTCAGAAACC	TACTCAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	300
CTCTGCATTA	AATCTATTG	CCATTCTGA	AAAAAAGAAA	AAAAAAGGG	CGGCCGCTCG	360
ANTCTAGAGG	GCCCGTTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCTTCT	ANTTGCCAGC	420
CATCTGTTGT	TTGCCCTCTCC	CCCGNTGCCT	TCCTTGACCC	TGGAAAGTGC	CACTCCACT	480
GTCCCTTCCT	AANTAAAAT					499

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAAATT	GGATTCA	GGCC	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAAGTAATAAG	GTAAAAGCTA	GTCTCTAA	CTACT	120
TCCAGGCCCA	CGGCTCAAGT	GAATTGAAAT	ACTGCATT	CAGTG	TAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGAACAG	TATTACAGTG	TCCTACC	ACT	TAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTGA	TGATTGAAATT	CTAAAAAATGG	TAATCATTAG	GGCTTTGAT	300
GGCTTTGAT	TTATAANACT	TTGGGTA	CTACTAAATT	ATGGTAGTTA	TACTGCCTTC	CAGTTGCTT	360
GATATATTG	TTGATATTAA	GATTCTGAC	TTATATT	AATGGGTTCT	ACTGAA	ACTGAA	420
ACTGAAAAN	GAATGATATA	TTCTGAAAGA	CATCGATATA	CATT	TATT	CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCC	CAAATTGTAT	GGT	GATAAAA	GTCCC	537

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATT	GGCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAAGG	AGGCCATCTT	TTCCCTCATCG	GTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTCT	GGGTTGGGC	CATTCA	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACCNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAACA	TCCCTGN		467

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60	
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAA	GATTCA	GGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATT	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180	
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAAAT	TGAAA	AAAGTG	GAGCATT	240
ACTGTCTTT	CAGCAAGGAC	TGGTCTTCT	ATCTCTGTA	CTACACTGAA	TTCACCCCCA	300	
CTGAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGT	CACAG	CCCAAGATNG	360

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT 400

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCCGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CGGCGGGGA TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAAAA	248

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTGC CGCTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GAAAACATT ATTATGTAAT TAATGTATGC TTTCTTGTMT ATAAATGCCT	180
GATTAAAAA AAAAAAAAAA A	201

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTGTTA TTACTTTCTT ATTCTTTATT	120
CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAGGTAG	180

TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAAACCTACT	300
CTGTCCTTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTTA	420
TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAAAAA AA	552

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TCGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCAAC TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTTAAACT TTCCCACCCA GAAAAGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300
TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TAAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAAAA AAAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCCTGGCTC TGCCCTCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACCTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC AGAAGCTAAA	GCCAAAGCCC AAGAAGAGTG	GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT	GCCAGTGCCA GTGCCAGCAC	CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCAGCCACT	CTCACATTTG GGCTCTTCGC	TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT	GGTGCCTGTG GTTCTCCTA	CAAGTGAGAT TTTAGATATT	240
GTAAATCTG CCAGTCTTTC	TCTTCAAGCC AGGGTGCATC	CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA	TCAATCAATT GAAGTTGACA	CTCTGCATTA AATCTATTTG	360
CCATTTCAAA	AAAAAAAAAA AAA		383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA	TCATGTCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG	GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA	CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC	CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA	ACCAAACCTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTTGCG AGCCATACTC TTTGGCNTCC	AGTCTCTCGT GGCGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA	GGGAACACAT TTGANTTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA	AATGAATTGA AAAACTCTTA	480
AAAAAAAAAA AAAA		494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGGANGG	GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC	TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC	AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCCTC CTGGGGCCCA GGCGGGCACC	TGGCTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG	GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC	AGGGCAACAG CNATCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG		380

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC CTCCACAACC	60
TNCATCGTC ATACTGAGG	120
GGAAACTCTC AATCAAGTCA	180
TGTGAAAGGA TCTCCAGAAC	240
GTCGATTCTG CATGTCCAGC	300
CTATCATGCC NTTGAACGTG	360
CCAGATTCTG CATTACCAGA	420
AAGAACACC TCCTGGAAGT	480
GCTNGCCGCT CCTCGTCCNT	
TGGTGGNNNGC GCNTNCCTTT	
T	481

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCCTGCTG AGAATTCA	60
ACTTGGAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTACAATA TGCAACACTT	120
TAAACAGTGT GTCAATCTGC TCCCCTACTT TGTCATCACC AGTCTGGAA TAAGGGTATG	180
CCCTATTACAC ACCTGTTAAA AGGGCGCTAA GCATTTTGAA TTCAACATCT TTTTTTTGAA	240
CACAAGTCCG AAAAAGCAA AAGTAAACAG TTNTTAATTGTTAGCCAAT TCACTTTCTT	300
CATGGGACAG AGCCATTGAA TTAAAAAGC AAATTGCATA ATATTGAGCTT TTGGGAGCTG	360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA	420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTT GTGGCAATTG TG	472

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCACT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTG AAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGCTCTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA	360
ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAACGTTTTTT TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CCGAGGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCCGCTG CTCCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCACTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAACNNNG	360
TTTACCAAGAA CCNAGCCAAT TNAGAACATT NCCCTCCAT AACAGCCCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTC TGCCAAAGTT GGTGTTGAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCGCTG TATTTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTCT GATGCGAAGT TCTNATTCCA GTGTTTGTAG CCTTGCATC	240
TTTNATGTTN AGACTTGCCT CTNTAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGTTN GAANATTGAA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTCNN	420
AATTCNNANA ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTCGCTGT	60
CTTCCACTCA	CTGTCCTGAA	GCTNTTAAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAAG	TCACATCTTC	TAGGACCTTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTTA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTG	TAGAAAGGAA	TTTAATGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTTA	AATTCTGCCA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGCTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCTCTTT	GACTACCGTG	TGCCAGTGT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACITG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAAGT	300
TGTCAAACT	AACCCGCTGG	TTTGCCTCCA	TCACATTTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCC	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCAC	CTGCTGAAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACTCCACT	CGTGGCTTG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAAGG	ATGCCCGACT	GTGCGGGACC	240
TGCAAGCAGAA	CTCCTCGATG	GTCATGAGCG	GGAAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACCGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCGGAGCA	CCCCCAGACC	GCTGCCGCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCTC	120
CGCCTCAATG	CAGAACCCANT	AGTGGGAGCA	CTGTGTTAG	AGTTAACAGGT	GAACACTGTN	180
TGATTTACT	TGGGAATTTC	CTCTGTTATA	TAGTTTTCC	CAATGCTAAT	TTCCAACAA	240
CAACACAAA	ATAACATGTT	TGCGCTGTNA	GTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAAA					377

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTGAGG	GGTTAGGGTC	CAGTCCCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCCA	TTCGGGGGCT	GTTCCTCCAG	GAGGAAGGG	AGGGGCTCTG	TGTGCCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300
TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAAC	CTTGCTNANA	480
AAAAAAAANA	AAAAAA					495

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC	60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT	120
TAGCTGTTTT GACTTGATT GCACCACTGC ACCACAACTC AATATGAAAA CTATTTNACT	180
TATTTATTAT CTTGTAAAAA GTATACAATG AAAATTGTTG TCATACTGTA TTTATCAAGT	240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA	300
ATCCGGCAAAA TGTTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCCTTT GTAACTTCAC	360
TTGGTTATT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA	420
TTTANTTCAN TAATTTCTTT CCTTGTAC GTTAATTG AAAAGAACATGC AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT	60
GTGGTGAAAT TTCAAAATTA TATGTAACCT CTACTAGTTT TACTTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT	180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNNGCANAATG TTCTAGNTAT	240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCAAAAT	300
TGTGTTAGTC TCAATTCTTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT	360
GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAGTN ACATCTGCGT	420
TACAAAGTCT ATCTTCCTCA NANGCTGTN AAGGAACAAT TTAATCTTCT AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 479 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA	60
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AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGCAAA TCAAAACTCA CAAGTGCCTCA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTPTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCACTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCTATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGGCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAG TTTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGCC TGGTTATCTA GATGAGAACAA GAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTGAATAA TCTTGACGCT CCTGAACCTG CTCCCTCTGCG A	461

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCCTCCCT	60
CGGGCGCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCCCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGA	GAGGTCTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAAC	GCAGGTGCAG	GTGGCCGCC				269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCA	TTTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGATTAG	GGTTCTTGC	CAAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TCACAAATGT	CTACAAATT	ATACCCATTA	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCCTTACCAA	ATAATACCCA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	240
CAAAGTACAA	TTATCTTAAAC	ACTGCAAACA	TTTTAAGGAA	CTAAAATAAA	300
CCGCAAAGGT	AAAGGGAAC	AAACAAATTCT	TTTACAACAC	CATTATAAAA	360
AAATCTTACGG	GGAAATATATA	CTTCACACGG	GATCTTAACT	ATCATATCTC	420
TTTAAACCA	TTGTTGGGC	CCAACACAAT	GGAATCCCCC	CTGGACTAGT	470

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTT	TTTTTTTG	CCCCCCTCTT	ATAAAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATCAAAAA	GCGAGCTTTT	AAAATCAAAC	120
TAATATGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
AAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATTC	240
ATTTTCTTG	TCTTAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTTCCIAAA	360
AGGGAAAACA	GGAAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATTCA	ATTTCTACCT	420
ACGTTAATAA	AATAGCATT	TGTGAAGCCA	GCTAAAAGA	AGGCTTAGAT	CCTTTTATGT	480
CCATTTAGT	CACTAACCGA	TATCAAAGTG	CCAGAACGCA	AAAGGTTGT	GAACATTAT	540
TCAAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTT	TTTTTCTCTT	CTTTTTTTT	GAAATGAGGA	TCGAGTTTT	60
CACTCTCTAG	ATAGGGCATG	AAGAAAAC	TC ATCTTCCAG	CTTTAAAATA	120
CTCTTATGCT	ATATCATATT	TTAAGTAAA	CTAATGAGTC	ACTGGCTTAT	180
AGGAAATCTG	TTCATTCTTC	TCATTCA	AGTATATCA	TGCATATTGA	240
GAGGTTTTTC	TTCTCTATT	ACACATAT	TTCCATGTGA	ATTTGTATCA	300
TTCATGCAA	CTAGAAAATA	ATGTTCTT	TGCATAAGAG	AAGAGAACAA	360
CAAATCTGCT	CAAATTGTTT	GTAAAGTTAT	CCATTATAAT	TAGTTGGCAG	420
AAATCACATT	TACGACAGCA	ATAATAAAAC	TGAAGTACCA	GTAAATATC	480
AAAGGAACAT	TTTACGCTG	GGTATAATT	GCTAATTAC	CAAATAATT	540
TGAATTCA	TGTTATTATT	CCTAGCCAA	CACAATGG		578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTAT	TTTTATAATT	AAAATT	CATA	60
GAAAGTGC	CC	TTACATTAA	TAAAAGTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAA	ACA	CCAATATTA	TTTGAGGAA	ATACACCAA	ATACATTAAG	AAATTATT	180
AAGATCAT	AG	CTTGTAAG	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCC	ACTA	TTAGCAAATA	AATTACTATG	GAAC	CTTGC	TTG TGATGAATAT	300
GGGGTGT	CAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTA	CTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTTCTTCAA	TCTTTAAGG	420
GGCGAGAA	AT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GT	TCTTCTA	480
AGATATGTT	C	CCTTGCCAA	TATTA	AAAAA	ATAATAATGT	TTACTACTAG	538

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTAGTC	AAGTTCTAT	TTTTATTATA	ATTAAGTCT	TGGTCATT	TC	60
ATTTATTAGC	TCTGCAACTT	ACATATTAA	ATTAAGAAA	CGTTT	TAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCA	TTATTGAGTA	ATATATTCT	CCAAGAGTGG	ATGTGTC	CCCT	180
TCTCCCACCA	ACTAATGAAC	AGCAACATTA	GT	TTAATT	TTT	ATTAGTAGAT	240
GCAAAACGCTA	ATTCTCTCT	CCATCCCCAT	GTGATATTGT	GTATATGTG	GAGTTGGTAG	300	
AATGCATCAC	AATCTACAA	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTT	CGGTGAAA	360	
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420	
CCGCTTCCTC	AAAGGCCGTG	CCACATTGT	GGCTCTTGC	ACTTGTTC	AAA	473	

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGGCA	TCTCGGT	CAT	GGAGCTGTCC	GGCCTGGCCC	CGGGCCC	GT	60
CTGTGCTATG	GT	CCCTGGCTG	ACTTCGGG	GC	GGTGTGGTA	CGCGTGGACC	GGCCCGG	120
CCGCTACGAC	GTGAGCCG	GT	GGCCGGGG	CAAGCG	CTCGTGT	ACCTGAAGCA	CT	180
GCCGCGGGGA	GGCCCG	GTG	GGCGGTCT	TG	CAAGCG	TGCTGGAGCC	240	
CTTCCGCGC	GGTGT	CAATGG	AGAAA	CTCA	GCTGGGCCA	GAGATTCTG	AGCGGG	300
TCCAAGGCTT	ATTTATG	GGCTGAGTGG	ATTG	GGCCAG	TCAGGAAGCT	TCTGCGG	TT	360
AGCTGGCAC	GATATCA	ACT	TTGGCTT	GT	CAGGTGTT	CTCT	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATG	CCC	CGCTGAATCT	CCTGG	GTCAC	TTTGCTGGT	GTGGC	480
GTGTGCACTG	GGCATTATAA	TGGCT	TTT	TGACCG	CACA	CGCACTG	CAGGT	540

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA	600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT	660
CTATACGACT TACAGGACAG CAGATGGGA ATTCACTGGCT GTTGGAGCAA TAGAACCCCA	720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT	780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAAGAC	840
GAAGGCAGAG TGGTGTCAAATCTTTGACGG CACAGATGCC TGTTGACTC CGGTTCTGAC	900
TTTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCAGTGA	960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCA CCATCCCTTC	1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTGGATT	1080
CAGCCGCGAA GAGATTTATC AGCTTAACCTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA	1140
ACCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG	1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTAA CAGTGTCTA	1260
CCACTCTAAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA	1320
AATGGTTATC ATTAGGGCTT TTGATTATAA AACTTTGGG TACTTATACT AAATTATGGT	1380
AGTTATTCTG CCTTCCAGTT TGCTTGAT ATTGTGAT ATTAAGATT TTGACTTATA	1440
TTTTGAATGG GTTCTAGTA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT	1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAT GCCACAAATT GTATGGTGAT	1560
AAAAGTCACG TGAAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1620
A	1621

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1           5          10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195         200         205

```

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210 215 220  
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
 225 230 235 240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245 250 255  
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Phe Ala  
 260 265 270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275 280 285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
 290 295 300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305 310 315 320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
 325 330 335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
 340 345 350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
 355 360 365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCCCTCT	ACCTGCCGA	CAGCTGGAAC	120
CAGTCGACCC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAATGGC	TGGTGGTGCT	GTCCTCGTC	600
ATCTTCCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	TTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGCGTC	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATTT	TCCGGGTTTA	CCTTCTAAG	GAAGCCGAGC	GGAAAGCTGCT	AACGTGGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGGA	GAGCGACTCC	960
GAGCGCTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTAGC	AACAGCGCCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGCGTC	1080
CTGGGGTGGG	TGGCCGGAGGC	CCTGAGCCGC	TCTGCCCTTGC	TGGCCCCCAGG	TGGGCCCCCA	1140
CCCCCTGACC	TGCGCTGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTTGCTCT	AGAGTAAGGC	TCATCTGGC	CTCGGGCCCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCG	GCTCCTCCCA	GAACCAAGTCC	CAGCCTGGGA	1380

GGATCAAGGC CTGGATCCCG GGCGTTATC CATCTGGAGG CTGCAGGGTC CTTGGGTAA	1440
CAGGGACAC AGACCCCTCA CCACTCACAG ATTCCCTACA CTGGGGAAAT AAAGCCATT	1500
CAGAGGAAAA AAAAAAAA AAAA	1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC CTGCACGCG TGGCTCCGGG TGACAGCCGC GCGCCTCGGC CAGGATCTGA	60
GTGATGAGAC GTGTCCCCAC TGAGGTGCCG CACAGCAGCA GGTGTTGAGC ATGGGCTGAG	120
AAGCTGGACC GGCACCAAAG GGCTGGCAGA AATGGGCAGC TGGCTGATT CTAGGCAGTT	180
GGCGGCAGCA AGGAGGAGAG GCCGAGCTT CTGGAGCAGA GCGAGACGA AGCAGTTCTG	240
GAGTGCTGAA ACGGCCCCCT GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG	300
GGTGAGCCGC CTGCTGCGGC ACCGGAAAGC CCAGCTTTG CTGGTCAACC TGCTAACCTT	360
TGGCCTGGAG GTGTGTTGG CCGCAGGCAT CACCTATGTG CCGCCTCTGC TGCTGGAAGT	420
GGGGGTAGAG GAGAAGTTCA TGACCATGGT GCTGGCATT GGTCAGTGC TGGGCCTGGT	480
CTGTGTCCTCG CTCCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCGCCGCG	540
GCCCTTCATC TGGGCAGTGT CCTTGGGCAT CCTGCTGAGC CTCTTCTCA TCCCAAGGGC	600
CGGCTGGCTA GCAGGGCTGC TGTGCCCCGA TCCCAGGCCC CTGGAGCTGG CACTGCTCAT	660
CCTGGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTGC TTCACTCCAC TGGAGGCCCT	720
GCTCTCTGAC CTCTTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCCTT	780
CATGATCAGT CTTGGGGGCT GCCTGGGCTA CCTCCTGCCT GCCATTGACT GGGACACCAG	840
TGCCCTGGCC CCCTACCTGG GCACCCAGGA GGAGTGCCTC TTTGGCCTGC TCACCCCTCAT	900
CTTCCTCACC TGCGTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAGCGC TGGGCCAAC	960
CGAGCCAGCA GAAGGGCTGT CGGGCCCCCTC CTTGTCGCC CACTGCTGTC CATGCCGGC	1020
CCGCTTGCT TTCCCGAACCG TGGGCGCCCT GCTTCCCCGG CTGCAACCGAGC TGTGCTGCG	1080
CATGCCCGC ACCCTGCGCC GGCTCTTCGCT GGCTGAGCTG TGCACTGGA TGGCACTCAT	1140
GACCTTCACG CTGTTTTACA CGGATTTCTGT GGGCGAGGGGG CTGTACCAAGG GCGTGCCCCAG	1200
AGCTGAGCCG GGCACCGAGG CCCGGAGACA CTATGATGAA GGCCTTCGGA TGGGAGCCT	1260
GGGGCTGTTGCT CTGCACTGCG CCATCTCCCT GGTCTTCTCT CTGGTCTGAG ACCGGCTGGT	1320
GCAGCGATTG GGCACCTCGAG CAGTCTATTT GGCCAGTGTG GCAGCTTCC CTGTCGGCTGC	1380
CGGTGCCACA TGCCTGTCCTC ACAGTGTGGC CGTGGTACAGA GCTTCAGCCG CCCTCACCGG	1440
GTTCACCTTC TCAGGCTCTGC AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA	1500
GAAGCAGGTG TTCCCTGCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG	1560
CCTGATGACC AGCTTCTCTGC CAGGCCCTAA GCCTGGAGCT CCCCCTCCATA ATGGACACGT	1620
GGGTGCTGGA GGCAGTGGCC TGCTCCCAAC TCCACCCGGC CTCTGCGGGG CCTCTGCTG	1680
TGATGTCCTCC GTACGTGTGG TGGTGGTGA GCCCACCGAG GCCAGGGTGG TTCCGGGCC	1740
GGGCATCTGC CTGGACCTCG CCATCCTGGA TAGTGCCTTC CTGCTGCTCC AGGTGGCC	1800
ATCCCTGTT ATGGGCTCCA TTGTCAGCT CAGCCAGTCT GTCACTGCCT ATATGGTGT	1860
TGCCGAGGC CTGGGTCTGG TCGCCATTAA CTTTGCTACA CAGGTAGTAT TTGACAAGAG	1920
CGACTTGGCC AAATACTCAG CGTAGAAAAC TTCCAGCACA TTGGGGTGA GGGCCTGCT	1980
CACTGGTCC CAGCTCCCCG CTCCCTGTTAG CCCCATGGGG CTGCCGGGCT GGCCGCCAGT	2040
TTCTGTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGTGCTGCT GAGGTGCGTA	2100
GCTGCCACAGC TGGGGGCTGG GGCCTCCCTC TCCCTCTCTCC CAAGTCTCTA GGGCTGCC	2160
ACTGGAGGCC TTCCAAGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCCA GAAGGGCTCC	2220
ATGCACTGGA ATGCGGGGAC TCTGCAGGTG GATTACCCAG GCTCAGGGTT AACAGCTAGC	2280
CTCCTAGTT AGACACACCT AGAGAAGGGT TTTTGGGAGC TGAATAAACT CAGTCACCTG	2340
GTTCCTCCATC TCTAAGCCCC TTAACCTGCA GCTTCGTTTA ATGTAGCTCT TGCACTGGAG	2400
TTTCTAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTG TAGGGGAAGA	2460
GTCCTGAGGG GCAACACACA AGAACCAAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT	2520

GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTGCCATCA	2580
CAGAGACACA GGCATTTAAA TATTTAACCT ATTTATTTAA CAAAGTAGAA GGGATCCAT	2640
TGCTAGCTT TCTGTGTTGG TGTCTAATAT TTGGGTAGG TGGGGGATCC CCAACAATCA	2700
GGTCCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCCTGGGT	2760
CTGGCCCCCCC AAAATGCCTA ACCCAGGACC TTGAAGAATT TACTCATCCC AAATGATAAT	2820
TCCAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTGGGCCAG CCTGGTTCCC CCCACITCCA	2940
CTCCCCCTCA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCCTACC	3000
CCCAACTTTC CCCTACCCCCC AACTTCCCG ACCAGCTCCA CAACCTGTGTT TGGAGCTACT	3060
GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTG TCCATCTCAG CCCCCCAGAGT	3120
ATATCTGTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGGTTTAAGT GCCGTTGCA ATAATGTCGT CTTATTTATT	3240
TAGGGGGTG AATATTTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA	3300
AAATAAAGG CTTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3360
AAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCCT GCCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCTTT	60
GTGGAGCCTC AGCAGTCCCC TCTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA	120
CCATGCAGTG CTTCACTTC ATTAAAGACCA TGATGATCCT CTTCAATTG CTCATCTTTC	180
TGTGTGGTGC AGCCCTGTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCGCAGC CGGCGTTGTG GTCTTGCTC TTGGTTCCCT GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCCTCATC TTCATTGCTG	420
AGGTGTCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACCAC CATGAAAGGG CTCAGTGTG GTGGCTTCAC CAACTATACG GATTTGAGG	600
ACTCACCCCTA CTTCAAAAGAG AACAGTGCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAAA GTAGAGGGTT	720
GCTTCATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACCTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACT GTGAAGAGGC	900
ACCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA	960
GAATGGACCT GCCCTTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACCT CCTTTTAGCG	1020
ATGCTGACT TTCTTCCAT TGGTGGTGG ATGGTGGGG GGCATTCCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACCC CTTGATATGC CCCCTAGGCC	1140
TAGGGTGAT CCCAGTGCCT TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT	1200
AAGTGAATC AGCAGGCCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAAA TGCATAAAC	1260
TGTTACAATG TTAAAAAAA AAAAAAAAAA	1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln  
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe  
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala  
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu  
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro  
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser  
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys  
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe  
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe  
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln  
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr  
210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290                    295                    300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305                    310                    315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 553 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1                5                    10                15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20                25                    30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35                40                    45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50                55                    60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65                70                    75                80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85                90                    95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100                105                    110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115                120                    125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130                135                    140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145                150                    155                160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165                170                    175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180                185                    190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195                200                    205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530                    535                    540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545                    550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
1                    5                    10                    15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
20                    25                    30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
35                    40                    45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
50                    55                    60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
65                    70                    75                    80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile  
85                    90                    95

Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
100                    105                    110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
115                    120                    125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
130                    135                    140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
145                    150                    155                    160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
165                    170                    175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
180                    185                    190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
195                    200                    205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
210                    215                    220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225                    230                    235                    240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCTC TCCCTCCTC TGAATTTAAT TCTTCAACT TGCAATTGCG AAGGATTACA	60
CATTTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAA GTGCTTTGT TTAAATTAC	120
TTGGTTTG TG AATCCATCTT GCTTTTCCC CATTGAACT AGTCATTAAC CCATCTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT	240
TCTCAGAACC ATTCACCCA GACAGCCTGT TTCTATCCTG TTTATAAAAT TAGTTGGGT	300
TCTCTACATG CATAACAAAC CCTGCTCAA TCTGTACAT AAAAGTCTGT GACTTGAAGT	360
TTAGTC	366

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTTCT ATATTATAGC AAAATTTAAA TCTACCCGTA TTCTAATATT	60
GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTTCATAT TTTAAGACAC ATGATTATAC CTATTTAGT AACCTGGTTC	180
ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	282

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAATTCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGAA TCTCTGATTC CCGCACAAATC TGAGTGGAAA	60
AANTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAAATTGGC CAACTTCTA TNAACATTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAAT AAAAGAAAAT TGAAAGGTTT CTCACTAACN GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAATGGAG AANCCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAGG T	171

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTC ATTCTCTTGG	120
TTAAGATTG T	131

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTGAGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACCA AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACATTG AATAGAAAA TAGAAACTGA GCTGAAATTT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTCCCCC CCAGGGATCA CCAAATATTT ATAAAATTT GT	112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTTCTAA TGTCTCCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTITG GGGACCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTCCCTTT TCCTAGCCTT	240
TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTTGTATC ACTCTGACTT TTTAGCATAAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACTC	120

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCCTCACG TTGGCCAATG	180
GATAAACAAA GT	192

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTATTG TGTGTTGCCG ATCTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTG CATTGGTAA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCCTCCAG GTTCGCCCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCATCTG TTATCACTGG AGAAAGCCA GACTCCCCAN GACNGGTACG GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAACTCGAT	TTCAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTTG	TATCTCGGGT	180
TTTAGCAAGT	AAAAATGAAN	ATGACAGGAA	AGGCTTATTT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAAC	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGGAAGCCT	300
GTAACAATCT	ACAAATTGGTC	CA				322

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTAT	CTGCATAATT	60
CTTGTCCCC	TTTCCATCTG	GCTCCTGGGT	TGACAATTTG	TGGAAACAAC	TCTATTGCTA	120
CTATTTAAAA	AAAATCACAA	ATCTTTCCCT	TTAAGCTATG	TTNAATTCAA	ACTATTCCCTG	180
CTATTCTGT	TTTGTCAAAG	AAATTATATT	TTTCAAAATA	TGTNTATTTG	TTTGATGGGT	240
CCCACGAAAC	ACTAATAAAA	ACCACAGAGA	CCAGCCTG			278

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA	CTTGTAGC	TCCATAGAGG	AAAGAATGTT	AAACTTTGTA	TTTTAAAACA	60
TGATTCTCTG	AGGTTAAACT	TGGTTTCAA	ATGTTATTTT	TACTTGTATT	TTGCTTTGG	120
T						121

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAATC CCTCAAAGAA CATCACTATA ACC	60
ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCAAG CTGGCACATT ACTTGTGTGC	120
AAACTTGATA CTTTGTCTCT AAGTAGGAAC TAGTATACAG TNCCCTAGGAN TGGTACTCCA	180
GGGTGCCCGG CAACTCCTGC AGCCGCTCT CTGTGCCAGN CCCTGNAAGG AACTTCGCT	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG	300
TTCCCAAGGA TGCAAAGCCT GGTGCTAAC TCCTGGGGCG TCAACTCAGT	350

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCCTGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG CCTTCTTCCT TTGTGGTGA CAACNCCAAG	240
AAAACTGCAG AGGCCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC	300
TCCCAGGAAC CGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT	399

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT	165

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACCTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAAACAGCC ACATGCCCAA	120
TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGGA GGGCTGGGGG CATANANGGT	240
CANGCTCAG GAAGCCTCAA GTTCCATTCA GCTTGCAC TGACATTCC CCATNTTAA	300
AAAAACTGAT GCCTTTTTTG TTTTTTTTG TAAAATTC	338

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCAGGAA GTGAAGGAGA	120
ATTCAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180
ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGGAAC TGTAAAGT GT	382

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATT	180
ATATTCAAGCA TAAAGGAGAA	200

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTCGA AAAAACACAT AGAAAAATAA AGTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGTGA	180
AATGGTTCTG AGAACCCATCC AATTCACTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG	300
ATTACACAAAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAACAGA CGTGTATTTA	60
GGGTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAACACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGTC	240
TTCAACACATC ATAGCCAATG ATGCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCACTG CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCCCT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

## (2) INFORMATION FOR SEQ ID NO:145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACCTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGAT ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCAG	240
TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC ATTAGAACAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTG GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGGCCC CTGGGCTGTG CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGUTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCT TATCTCATCG AATTTTTAAC CCAAACATCAC TCACGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCA TCCANGCCTG CACCTTGAGC CTTTGAGCTC CATTGCTCAC	240
NCCANCCCAC CTCACCGACCC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCCA	300
TAGATTATNT CCAAATTCA TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120

GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAAC	180
TTTCAGGCAG AGGAAACAGC AGTGAAA	207

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGTATT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T	111

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCGAG	120
GAGGGAGTTT GT	132

## (2) INFORMATION FOR SEQ ID NO:153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTATGGCC TCCAAACATG AAAGTGTCA	60
CTTCTGCTCT TATGTCTCA TCTGACAAC TTTTACCAT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCAC ACGGAGTNAG GAATT	285

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTAAAC TGAAGGGTC AGCCTTGTGA CTGCAAAGAC	120
CCTAACGCCG TTACACAGCT AACTCCCCTGATT TGTGAAATTG CTGCTGCCCTG	180
ATTGGCACAG GAGTCGAAGG TGTCAGCTC CCCTCCCTCG TGGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACTGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCTGC CTGCTCCTCC TGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGCTGATT CTTCTGGCT	240

GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AAGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAAGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCCTGGCT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTG TGTAAGGAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGTAA TTCACCATTA ATTCCTCCC CCAAACCTTC TGAGTCTTCC CTTAATATTT	180

100

CTGGTGGTTC TGACCAAAGC AGGTCAATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATTTTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCTGT TTTCCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTTGCGAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTCCT CGATGTCCT GT	442

## (2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTTC	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACAGGCCAAAG GTTGTGGAAC TGGCANAAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGGCGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGC	240
TGCTGTTGTT CCGGGGAGNTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGAAAGT	300
ANTANATTCT TCCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTGN	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCACC	480
AAGGGATAAA GCTGTGGT	498

## (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC	240
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTG TAACATCCTG	300
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

## (2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 114 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA	60
GTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTTAAT GAGGGAGTTC CAGGAGATT CACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAAC TG CCAAAGAAC TTCAAGAAGG AGGACTGCAA GTATATCGT	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCTAT CAGTAAAAAG ATNTTGAGC AACACATT	469

## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CGGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGAGG TGTGCTCAAT CTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACCC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGCCTTT TTGGTGAAC TTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAACGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC CTACCACAAA AACAAATAGGA TCACTGCTGG GCACCCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCGTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACCGG CGAGGACTGC AGCCCGACT CGCAGCCCTG GCAGGCGGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCCTCTGG TGCTCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCTG	180
CACAGCTTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CGGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC	360
GCGGGAACT CTTGCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC	420
GTGCTGCACT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCAGGGGC AAAGACCAGAA GGACTCCTGC	540
AACGGTGAAT CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAGGGCCT TGTGTCTTC	600
GGAAAAGCCC CGTGTGGCCA AGTTGGCTGT CCAGGTGTCT ACACCAACCT CTGCAAATTC	660
ACTGAGTGGG TAGAGAAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA	720
ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCCT	780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCCTCCC TCAAACCAAG GGTACAGATC	840
CCCAGCCCC CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC	900
CCAGGAGTCC AGCCCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC	960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCCTCCCTC AGACTCAGAG GTCCAAGCCC	1020
CCAACCCNTC ATTCCCCAGA CCCAGAGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA	1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC	1140
AACCTTACCA GTGGGTTTTT CATTTTNGT CCCTTCCCC TAGATCCAGA AATAAAGTTT	1200
AAGAGAAGNG CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro		
1																	
														15			
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser		
														20	25	30	
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr		
														35	40	45	
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly		
														50	55	60	
Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu		
														65	70	75	80
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe		
														85	90	95	
Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser		
														100	105	110	
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe		
														115	120	125	
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn		
														130	135	140	
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser			
														145	150	155	

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGCG	GCAC TGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGGGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCTTGCT	CGCTAACGAC	240

CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCTAC	CGCGGGAAAC	TCTTGCCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGCTG	CCCTCTTCAA	GGAGGTCTCTG	TGCCAGTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCAACCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCGTGTAT	CTGCAACGGG	TACTTGCAGG	GCCTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	C GTGCCAGGG	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720
AAACCGTCCA	GGCCAGTAA	CTCTGGGGAC	TGGAAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCGTGCGGA	AGGAATTCAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGGCCCC	CAGCCCTCC	TCCCTCAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCCTCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGGTT	1020
GAGGGCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAAA						1265

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAAGAGCT	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCCTGC	TGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCGAGTCT	GACACCATCC	GGAGCATCG	CATTGCTTGC	CAGTGCCTA	240
CCGCGGGAA	CTCTTGCCTC	GTTCCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGCT	GCCCTCTTCA	AGGAGGTCT	CTGCCCCAGTC	GGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCC	GGCAGAAATGC	CTACCGTGC	GCAGTGCCTG	AACGTGTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGGCACT	540
CAGGGAAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAAACAGAC	ATGGGGAGGC	720
AGAAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAAA	T CCTTCTATA	ACTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTCAGGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATTT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTTGAT	ATTTCTAACG	TACACAGTTC	960
GTCTGTGAAT	TTTTTAAAT	TGTTGCAACT	CTCTTAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTG	ATAGAGGTGA	AAACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGCAG	GGTGGCTCAT	GCCTGTAAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTAGCTGG	ATATGGTGGC	AGGCGCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCGAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGCC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAAAAAA	AAAAAAAAAA					1459

## (2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCGAGCCCT	GGCAGGCCGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGGA	GCCAGATGGT	GGAGGQCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300
TGCCCCTACCG	CGGGGAACCTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGGTG	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCCTGCA	ACGGTGAETC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAAAC	GTCCAGNCCA	TTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATAACATCT	GCGGAANGAA	TTCAAGGATA	TCTGTTCCCA	720
GCCCCCTCTC	CCTCAGGCCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTTCCCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAACGCC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Lle	Phe	Cys	Ser	Gly	Val	Lle	Val	His	Pro	Gln	Trp
1				5				10				15			
Val	Lle	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Lle
				20			25				30				
Gly	Lle	His	Ser	Lle	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35			40				45				
Glu	Ala	Ser	Lle	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Lle	Lle	
				50			55				60				

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65                    70                    75                    80  
  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85                    90                    95  
  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100                  105                  110  
  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115                  120                  125  
  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130                  135                  140  
  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145                  150                  155                  160  
  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165                  170                  175  
  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180                  185                  190  
  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195                  200                  205

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCAC TG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGACTAC	AACAGACCCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGGCAGTGCC	CTACCGCGGG	GAACCTTG	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATCCTGTGA	TTGCCATCCA	GTCCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTCC	420
CAACCCCTGGC	AGGGTTGTAC	CATTTCCGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480
CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGGAA	CACTGTGATC	AACTAGCCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTGC	TGTCTATITGT	600
ACTAACCATG	CCGATGTTTA	GGTGAAATTA	GCGTCACTTG	GCCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTTCTG	CTTCAGTGTGTC	AGCCATTCCC	ACATAATTTC	720
TGACCTACAG	AGGTGAGGG	TCATATAGCT	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCACTTCTC	CTGTTGTAGT	GAAAGGTGCC	CCCTCTGGAG	CCTCCCAGGG	TGGGTGTGCA	840
GGTCACAATG	ATGAATGTAT	GATCGTGTTC	CCATTACCCA	AAGCCTTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTTTC	TTCACTTGTAGT	GTATGCTGTC	CATTCAATGCA	960
ACCACCTCAG	GACTCCTGGA	TTCTCTGCCT	AGTTGAGCTC	CTGCATGCTG	CCTCCTGGG	1020
GAGGTGAGGG	AGAGGGCCCA	TGGTTCAATG	GGATCTGTGC	AGTTGTAACA	CATTAGGTGC	1080

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1		5							10					15	

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
	20						25						30		

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
	35				40							45			

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
	50				55						60				

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
65				70			75					80			

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
	85				90						95				

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
	100				105						110				

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
	115				120						125				

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
130				135							140				

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
145				150						155			160		

Pro Gly Thr Leu

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60

110

CCAGCTGCC	CCGGCCGGGG	GATGCGAGGC	TCGGAGCACC	CTTGGCCGGC	TGTGATTGCT	120
GCCAGGCACT	GTTCATCTCA	GCTTTCTGT	CCCTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTCATAT	CTGGAGCCTG	ATGTCTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAA	240
AAAAAAAAAA						250

## (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCAA	CACAATGGCT	ACCTTTAACCA	60
TCACCCAGAC	CCCGCCCCCTG	CCC GTGCC	ACGCTGCTGC	TAACGACAGT	ATGATGCTTA	120
CTCTGCTACT	CGGAAACTAT	TTTTATGTAA	TTAATGTATG	CTTTCTTGTT	TATAATGCC	180
TGATTTAAAA AAAAAAAAAA AA						202

## (2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT	NAGGTTTKKG	AGACAMCCCK	AGACCTWAAN	CTGTGTCACA	GACTTCYNGG	60
AATGTTAGG	CAGTGCTAGT	AATTCYTCG	TAATGATTCT	GTTATTACTT	TCCTNATTCT	120
TTATTCTCT	TTCTTCTGAA	GATTAATGAA	GTTGAAAATT	GAGGTGGATA	AATAACAAAA	180
GGTAGTGTGA	TAGTATAAGT	ATCTAAGTGC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATTATGCA	AGTTAGAAT	TACTCAGGGT	TAAC TAAATT	ACTTTAATAT	GCTGTTGAAC	300
CTACTCTGTT	CCTTGGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTTC	AAAAAGTTGG	GCTATACATA	AATTATTAAG	AAATATGGAW	420
TTTTATCCCC	AGGAATATGG	KGTTCAATT	ATGAATATTA	CSCRGGATAG	AWGTWTGAGT	480
AAAAYCAGTT	TTGGTWAATA	YGTWAATATG	TCMTAAATAA	ACAAKGCTTT	GACTTATTTC	540
CAAAAAAAAAA AAAAAAAAAA						558

## (2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK	GRGGATGCTA	AGSCCCCRGA	RWTYGTGTTGA	TCCAACCCCTG	GCTTWTTTTC	60
AGAGGGAAA	ATGGGGCCTA	GAAGTTACAG	MSCATYTAGY	TGGTGCGMTG	GCACCCCTGG	120
CSTCACACAG	ASTCCCGAGT	AGCTGGGACT	ACAGGCACAC	AGTCACTGAA	GCAGGCCCTG	180
TTWGCAATT	ACGTTGCCAC	CTCCAACTTA	AACATTCTTC	ATATGTGATG	TCCTTAGTCA	240
CTAAGGTTAA	ACTTTCCCAC	CCAGAAAAGG	CAACTTAGAT	AAAATCTTAG	AGTACTTTCA	300
TACTMTCTA	AGTCCTCTTC	CAGCCTCACT	KKGAGTCCTM	CYTGGGGGTT	GATAGGAANT	360
NTCTCTTGGC	TTTCTCAATA	AARTCTCTAT	YCATCTCATG	TTAATTG	TACGCATARA	420

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAAA ARAAAAAAAA AAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC AGAACGCTAAA	GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCATAAACAG TGCCAGTGC	AGTGCAGCA CCAGTGGTGG CTTCACTGCT	120
GGTGCAGCC TGACCGCCAC	TCTCACATTG GGGCTCTCG CTGGCCTTGG TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC	TGGTGCCTGT GGTTTCTCCT ACAAGTGAGA TTTTAGATAT	240
TGTTAATCCT GCCAGTCCTT	CTCTTCAGAC CAGGGTGCAT CCTCAGAAC CTACTCAACA	300
CAGCACTCTA GGCAAGCCACT ATCAATCAAT	TGAAGTTGAC ACTCTGCATT ARATCTATT	360
GCCATTCAA AAAAAAAA AAAA		384

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYNT CCRGTATKAC	CTCAACGAGC	60
AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG		120
CCCATCCTGC TCGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA		180
AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGGGCCCTGT CCTCTGAGGG TCCCCTTAAC		240
TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG		360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT ATTAAAATT ACTACMAGAW TATTWMAW WAAATGAWTT GAAAAACTST		480
TAAAAAAA AAAA		496

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC		60
CAAGTATCYT GGGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC		120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAAATG YTCGTCGGAG CCCGGCTTCT		180
GGGCACACCC TCCGGGGCC CAGGGGGCA CCTGGCTCTC CCAGTATGCC AACTGGCTGG		240
TGGTGTGCT CCTCGTCATC TTCTGCTCG TGGCCAAACAT CCTGCTGGTC AACTTGCTCA		300
TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG		360
GCGCAGCGTT ACCGCCTCAT CCGG		384

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATAACCGC	60
TNCCATCGTC	ATACTGTAGG	TTGCCACCA	CYTCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCAACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGGCAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAG	ACATTGACAA	ACTCGECCAG	420
GTGGAAAAAG	AMCAMCTCCT	GGARGTGCTN	GGCGCTCCTC	GTCMGTGTT	GGCAGCGCTW	480
TCCTTTGAC	ACACAAACAA	GTAAAGGCA	TTTCAGCCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAT			577

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCGTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCAACAT	ATGCAACACT	120
TTAACACAGT	TGTCAATCTG	CTCCCCYNAC	TTTGTCATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTG	ACACCTGTTA	AAAGGGCGCT	AAGCATTGTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAAAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATTY	GATTTAAAAA	GCAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGAG	GCGGAAGAGT	AGCCTTCTA	CTTCACCCAGA	CACAACCTCC	TTTCATATTG	420
GGATGTTMAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCCT	TTTCTTCCTC	AGGC	534

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTGTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGCGCG	CGCATATTAT	ATAGACAGGC	ACATTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGCTCTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACATWA	CCTGGTGAGA	ARTTGCTAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTCTCCCTT	420

GCAAAAAACA TGTACNGACT	TCCC GTTGAG TAATGCCAAG TTGTTTTTTT TATNATAAAA	480
CTTGCCTTC ATTACATGTT	TNAAAGTGGT GTGGTGGGCC AAAATATTGA AATGATGGAA	540
CTGACTGATA AAGCTGTACA	AATAAGCAGT GTGCCAACAA AGCAACACAG TAATGTTGAC	600
ATGCTTAATT CACAAATGCT	AATTCATTA TAAATGTTG CTAAAATACA CTTTGAAC	660
TTTTCTGTN TTCCCAGAGC	TGAGATNTA GATTTATGT AGTATNAAGT GAAAANTAC	720
GAAAATAATA ACATTGAAGA	AAAANANAAA AAANAAAAAA A	761

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT TTTGCCGATN	CTACTATTTT ATTGCAGGAN GTGGGGGTGT ATGCACCGCA	60
CACCGGGCT ATNAGAAGCA	AGAAGGAAGG AGGGAGGGCA CAGCCCTTG CTGAGCAACA	120
AAGCCGCTG CTGCCTTCTC	TGTCTGTCTC CTGGTGCAGG CACATGGGGA GACCTTCCC	180
AAGGCAGGGG CCACCAGTC	AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG	240
TGATAGGCAC AGGCCACCCG	GTACAGACCC CTCCGCTCCT GACAGGTNGA TTTCGACCAG	300
GTCATTGTGC CCTGCCAGG	CACAGCGTAN ATCTGGAAAA GACAGAATGC TTTCTTTTC	360
AAATTGGCT NGTCATNGAA	NGGGCANTTT TCACANTTNG GCTNGGTCTT GGTACNCTTG	420
GTTCCGGCCA GCTCCNCGTC	CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCGNGNCCC	480
CC		482

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT TTTAAAACA	GTTCACACA ACAAAATTAA TTAGAAGAAT AGTGGTTTG	60
AAAACCTCTG CATCCAGTGA	GAACCTACCAT ACACCACTT ACAGCTNGGA ATGTNCTCCA	120
AATGTCTGGT CAAATGATAC	AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAAG	180
CGCTTTGAC ATACAATGCA	CAAAAAAAA AGGGGGGGGG GACCACATGG ATTAAAATT	240
TAAGTACTCA TCACATACAT	TAAGACACAG TTCTAGTCCA GTCNAAATC AGAACTGCNT	300
TGAAAAATTAA CATGTATGCA	ATCCAACCAA AGAACTTNAT TGGTGTATCAT GANTNCTCTA	360
CTACATCNAC CTTGATCATT	GCCAGGAACN AAAAGTTNAA ANCACNCNGT ACAAAANAA	420
TCTGTAATTN ANTCAACCT	CCGTACNGAA AAATNTNNNT TATACACTCC C	471

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTT	TASTGTCGGM CTGTTAGCC ACCAACTCTA ACAAGTGCT	60
GTCTTCCACT CACTGTCTGT	AAGCTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA	120

ATTCTTCACC AGTCACATCT TCTAGGACCT TTTGGATTC AGTTAGTATA AGCTCTTCCA	180
CTTCCTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTTAGAAAGG AATTYAATTG	240
CTCGTTCTCT ACAATGTCC TCTCCTTGAAT GTATTTGGCT GAACAACCCA CCTAAAGTCC	300
CTTTGTGCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC	360
AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA	402

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT CCAATAATCT TTGCTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC	120
ATGCYTYTTT GAYTACCGTG TGCCAAGTGC TGGTGATTCT YAACACACYT CCATCCCGYT	180
CTTTTGTGGA AAAACTGGCA CTTKTCTGGA ACTAGCARGA CATCACTTAC AAATTCACCC	240
ACGAGACACT TGAAAGGTGT AACAAAGCGA YTCTTGATT GCTTTTGTC CCTCCGGCAC	300
CAGTTGTCAA TACTAACCCG CTGGTTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA	360
TACATCTCCT GACAGTACTG AAGAACTTCT TCTTTGTTT CAAAAGCARC TCTTGGTGCC	420
TGTTGGATCA GGTTCCCATT TCCCAGTCYG AATGTTCACA TGGCATATTT WACTTCCCAC	480
AAAACATTGC GATTTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATTG GCTGCAAGAG	540
CCTCGATGTA GCCGGCCAGC GCCAAGGCAG GCGCCGTGAG CCCCACCAAGC AGCAGAAGCA	600
G	601

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCC NATCCCACCA CGAAAGATGCG CTTGTTGACT GAGAACCTGA TGCGGTCACT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCYTT	120
CCCAACGCG GCGAGMAGCGG GSCCGGTCAA TGAACCTCCAY TCGTGGCTTG GGGTKGACGG	180
TKAAGTGCAG GAAGAGGCTG ACCACCTCGC GGTCCACCAG GATGCCCGAC TGTGCGGGAC	240
CTGCAGCGAA ACTCCTCGAT GGTCTGAGC GGGAAAGCGAA TGAGGCCAG GGCCTTGCCC	300
AGAACCTTCC GCCTGTTCTC TGGCGTCACC TGCAGCTGCT GCCGCTGACA CTCGGCCTCG	360
GACCAGCGGA CAAACGGCRT TGAACAGCCG CACCTCACGG ATGCCAGTG TGTGCGCTC	420
CAGGAMMGSC ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCCTCCGGG GTRATGGCGT	480
CTGCAGTGT TTTGTCGATG TTCTCCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA	540
GTCGCGCCTG CGTGAGCAGC ATGAAGGCAGT TGTCGGCTCG CAGTTCTTCT TCAGGAACTC	600
CACGCAAT	608

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCTC	GCATTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCGAG	CAGCCCCAGA	CCGCTGCCG	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCTCTAA	TGCAAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGTATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAC	240
AACAAACAACA	AAATAAACATG	TTTGCTGTT	AAAGTTGTATA	AAAGTAGGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAAAT	AGTTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGGTGT	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAAGGC	CCCATTCCGG	GGSTGTTCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCCTCTCA	GTCCCCCTTC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGG	GA	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	480
GCTNAAAAAA	AAAAA	AA				502

## (2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAAG	CCTTGCAG	AGCGGACTTT	GTAAATTGTTG	GAGAATAACT	GCTGAATTTC	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAT	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAAGTATGATG	AAAAGCAAWA	GATATATAATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTTCACAGT	AATATATGCC	TTTTGTAAC	360
TCACCTGGTT	ATTTTATTGT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTATT	TCATTAATT	CTTTCCCTKGT	TTACGTTWAAT	TTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTAAAGAT	GTATAAAGGT	TGTAGCCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
						665
AAGTG						

## (2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTNTTTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCACTGA	AAAGTATCAA	GTGTTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTCT	GAACTTAGA	TTTCTAGAA	AAATATGTA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTG	ATTCANTCT	GTANNAANTA	TTTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNCTGAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTCA	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTCTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNNG	CCGTTTANTG	420
AACNTNGACN	NCACCCCTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGGCGCAAG	TGCAACTCCA	GCTGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	CGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCGCA	GAGGTGGTGT	CACGTCCAC	GACCTTGACG	CCGTCGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAANGGGGA	GGCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCGCC				270

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTGGAACATC	TACTGCGAGC	ACAGCAGGTC	ACGACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTAG	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAC	ANAANTAAACA	180
TGGAGTGGGT	GCACCCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTTCTT	GACATCAATG	TTATTAGAAAG	TCAGGATATC	TTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTTA	TTTCAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNATTTCNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAA	AATCAAAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTNNA	300
GGAACTAAAA	AAAAAAAAAA	CACTNCCGCA	AAGTTAAAG	GGAACAAACAA	ATTCTNTTAA	360
CAACANCNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAAC	TTTACTNCA	CTTGTGTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAACAA	480
CAATGGNAAT	NCCNCCNCC	TGGACTAGT				509

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTG	CCCCCTCTT	ATAAAAAACA	AGTTACCAATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTT	AAAATCAAAC	120
TAATGGAAA	CTGCCCTAGA	TACATAATTC	TTAGGAATTA	GCTTAAATC	TGCCTAAAGT	180
GAAAATCTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAACAC	ATCCAAATTC	240
ATTTTCTTG	TCTTTAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTCC	AAGTCATTT	300
GCTTCTCTAG	CCTCATTTC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCTCTAAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTCAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTCTAG	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAAGGTTT	GTGAACATTT	540
ATCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTTT	CTG		583

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTNCTC	TTCTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	AGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTTAA	120
AAATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AAACTAATGA	GTCACTGGCT	180
TGAAGGAAAT	CTGTTCAITC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	300
ATTTTCATGC	AAACTAGAAA	ATAATGTTT	CTTTTGCATA	AGAGAAGAGA	360
CATTACAAA	CTGCTCAAAT	TGTTTGTAA	GNTTATCCAT	TATAATTAGT	420
CTAATACAAA	TCACATTTCAC	NGACNAGCAA	TAATAAAACT	GAAGTACCAAG	480
AAAATAATTA	AAGGAACATT	TTTACCTGG	GTATAATTAG	TTAAATATCC	540
TTATTNAGAA	TGAATTCA	TGTTTATTATT	CCNTAGCCC	ACACAATGG	589

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATTAA	TTTTTATATT	TAATTCAT	60
AGAAAAGTGC	CTTACATTAA	ATAAAAGTTT	GTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTGAA	CACCAATATT	AATTTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAACATCAT	AGAGCTTGTA	AGTAAAAGA	AAAATTGTA	CCTCAGAAC	TCTGAGCATT	240
AAAATCCAC	TATTAGCAA	AAAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGT	ACTGGTAAAC	CAACACATT	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTAATT	GCTANATNAC	GTGGATATGA	GTGACAAGT	TTCTCTTCT	TCATCTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGA	AAGGATTACG	CATACTGTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTCT	TTGCCAATAT	AAAAAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT TTTTTTAGTC AAGTTCTNA TTTTTATTAT AATTAAAGTC TTGGTCATTT	60
CATTTATTAG CTCTGCAACT TACATATTAA AATTAAAGAA ACCTTNTTAG ACAACTGTNA	120
CAATTATATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTCTCC ACCAACTAAT GAANCAGCAA CATTAGTTA ATTTTATTAG TAGATNATAC	240
ACTGCTGCAA ACGCTAATTCT TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG	300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT	360
TCGGTGAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATT GTGGCNTCTN TTGCACTTGT	480
TTCAAAA	487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAAA	60
TACATAGCAT TAAATCCCAA ATCCTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTTATAG GACCTTCTGG TGGTTCTGCT GTTACNTTTG AANTCTGACA ATCCCTGANA	180
ATCTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTCA CAGAGGAANA ACACACCGCA	240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGAGCC CA	332

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT GCGGAGGGCG TTACTGTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG	60
GTTGTGTTCC GGCCCCATCC AACCACGAAG TTGATTCTC TTGTGTGCAG AGTGAAGTGT	120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC	180
TCCCCCGTGA TTCACATTAA GCAACCAACA ATAGCTCATG AGTCCATACT TGAAATACT	240
TTTGGCAGAA TACTTNTTGA AACCTGCAGA TGATAACTAA GATCCAAGAT ATTTCCAAA	300
GTAAAATGAA GTGGGTCATA ATATTAATTA CCTGTTCACCA TCAGCTTCCA TTTACAAGTC	360
ATGAGCCCAG ACACTGACAT CAAACTAACG CCACCTAGAC TCCTCACCAC CAGTCTGTCC	420
TGTCAATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAATC ATCTATCCAA	480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA	524

(2) INFORMATION FOR SEQ ID NO:209:

120

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA	159

(2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAGTGCC	60
ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTGGA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGAAAA CAGAAAAAGA	240
AAAAAAAGGAG CAAATGAGAA GCCT	264

(2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTT GATTGTCAA	60
GGATTAAATG TTGTCAGC TTGGGACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCGCCAG	180
TTNAATTTCAGC TTCCCCATTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA	300
TTTTTTTTTC CTTTATTCCCT TTGTCAGA	328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACGTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTG ATTGTCAAAG	60
GATTTAATGT TGTCTCAGCT TGGGCACCTTC AGTAGGACC TAAGGATGCC AGCCGGCAGG	120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TTATTGAACTT GCCCGCCAGT	180
TGAATTTCAT TCCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC	240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT	300
TTTTTTTCC TTTATTCCCTT TGTCAAGAGT GCGATTCTCATC CATATGCTAN AAACCAACAG	360
AGTGAACCTTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT	420
ACTTGCTCT CCCTAATATA CCTC	444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAACGTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120

CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT	240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA	300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT	360
GGTGCC	366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAAC TCCGCTTGTC	60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTA GGGCTNTTNC ATTTTTTTAT	120
TAATAAAAAG TNNAAAAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA	180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT	240
AATTCTTCCT TCCCTCCCTT	260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTCAAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTTAT AATTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTAA	180
ATGAATAATC TGATGATTA TATGCTCTA GAGTAGATT ATAATTAGCC ACTTACCCCTA	240
ATATCCTTCA TGCTTGTAAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCGAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGNTNAA NGTCCAGGGT TGCTAGGAAA	180
ANAAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TAATGTTTGT TCTCACTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCCT TCATCTTGG A TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCC GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAGG GCCATACTGC ATAAAGTCAA CAACAGATAAA	120
ATGTTTGCTG AATTAAGGA TGGATAAAA AAATTAATAA TGAATTTTG CATAATCCAA	180
TTTTCTCTTT TATATTTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT	300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T 351

## (2) INFORMATION FOR SEQ ID NO:223

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTKT GGGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG TGTGCTATT	240
TAAAAGAGTT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG CGAAANAGTT	300
ATAGGACAC AGTCTTCACT TCTGATACTT GTAAATTAAAT CTTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.

3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.

4. An expression vector comprising the DNA molecule of claims 2 or 3.

5. A host cell transformed with the expression vector of claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.

7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.

8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.

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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> <b>PCT/US98/03492</b>		<b>(81) Designated States:</b> AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
<b>(22) International Filing Date:</b> <b>25 February 1998 (25.02.98)</b>		<b>(30) Priority Data:</b> 08/806,099            25 February 1997 (25.02.97)    US 08/904,804            1 August 1997 (01.08.97)        US 09/020,956            9 February 1998 (09.02.98)        US
<b>(71) Applicant:</b> CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		<b>(72) Inventors:</b> XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).
<b>(74) Agents:</b> MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).		<b>(88) Date of publication of the international search report:</b> <b>17 December 1998 (17.12.98)</b>

**(54) Title:** COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE**(57) Abstract**

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 98/03492

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6	C12N15/12	C07K14/705	C12N5/10	C12N1/21	A61K38/17
	C12N1/19	A61K39/00	C12N15/62		

According to International Patent Classification (IPC) or to both national classification and IPO

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	
A	WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document ---	
A	WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document ---	
A	EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document ---	
	-/-	

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

### \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

30 July 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

**INTERNATIONAL SEARCH REPORT**

Inten nal Application No
PCT/US 98/03492

**C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES"</p> <p>NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597</p> <p>see the whole document &amp; "AC No. AA453562"</p> <p>EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765</p> <p>---</p>	2,4-6
X,P	<p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)"</p> <p>EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072</p> <p>see the whole document</p> <p>-----</p>	2,4-6

**INTERNATIONAL SEARCH REPORT**Int'l. application No.  
PCT/US 98/03492**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:  
**Remark:** Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2.  Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3.  Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

**Remark on Protest**

- The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 15.

11. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 16.

12. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 17.

13. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 18.

14. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 19.

15. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 20.

16. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 21.

17. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 22.

18. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 23.

19. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 24.

20. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 25.

21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 26.

22. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 27.

23. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 28.

24. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 29.

25. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 41.

26. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 42.

27. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 43.

28. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 44.

29. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 45.

30. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 47.

31. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 48.

32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 49.

33. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 50.

34. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 51.

35. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 52.

36. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 54.

37. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 55.

38. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 56.

39. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 57.

40. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 58.

41. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 59.

42. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 60.

43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 61.

44. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 62.

45. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 63.

46. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 64.

47. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 65.

48. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 70.

49. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 73.

50. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 74.

51. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 79.

52. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 81.

53. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 87.

54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 90.

55. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 92.

56. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 93.

57. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 97.

58. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 103.

59. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 104.

60. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 107.

61. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 109.

62. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 110.

63. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 111.

64. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 115.

65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 116.

66. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 117.

67. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 118.

68. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 119.

69. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 120.

70. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 121.

71. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 122.

72. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 123.

73. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 124.

74. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 125.

75. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 126.

76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 138.

88. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 139.

89. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 140.

90. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 141.

91. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 142.

92. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 143.

93. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 144.

94. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 145.

95. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 146.

96. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 147.

97. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 148.

98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 152

102. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 155.

105. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 156.

106. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 6.

133. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 7.

134. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 30.

135. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 31.

136. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 32.

137. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 33.

138. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 34.

139. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 35.

140. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 36.

141. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 37.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

142. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 38.

143. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 39.

144. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 40.

145. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 46.

146. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 53.

147. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 66.

148. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 67.

149. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 68.

150. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 69.

151. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 71.

152. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 72.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

153. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 75.

154. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 76.

155. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 77.

156. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 78.

157. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 80.

158. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 82.

159. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 83.

160. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 84.

161. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 85.

162. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 86.

163. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 88.

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164. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 89.
165. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 91.
166. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 94.
167. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 95.
168. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 96.
169. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 98.
170. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 99.
171. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 100.
172. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 101.
173. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 102.
174. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 105.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

175. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 106.
176. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 161.
177. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 162.
178. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 163.
179. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 164.
180. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 165.
181. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 166.
182. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 167.
183. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 168.
184. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 169.
185. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 170.

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186. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 179.

187. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 180.

188. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 182.

189. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 183.

190. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 184.

191. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 185.

192. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 186.

193. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 187.

194. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 189.

195. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 190.

196. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 192.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

197. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 195.

198. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 196.

199. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 197.

200. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 199.

201. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 200.

202. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 201.

203. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 202.

204. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 205.

205. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 206.

206. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 208.

207. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 212.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

208. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 213.

209. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 214.

210. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 215.

211. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 216.

212. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 217.

213. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 218.

214. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 219.

215. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 221.

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